

CaI	PVAALKEKS-HTEKVQEALND-PKKHVIVAMAPSVRTAMGELFKMGYKGD	247
CpI	PVAALSEKS-HMDRKNALNA-PEKHVIVAMAPSVRASIGELFNMGFGVD	248
Dd	PENATYEAOQSWMPPEVEKKLKD-GAVKCIAMPAPAVRYALGDAFGMPVGSV	98
CrHydA2	ATDAMPHWKLAEEEDKPKDG-GRKVEIAQVAPAVRVAEAESEFGLAPGAV	113
CrHydA1	AEAPSHVQQATAEAKPKDDPTKHVCVQVAPAVRVAEATLGLAPGAT	110
CaI	VTCQYTAEMCPDKVYDINGCMLDQVAAEAEFEGK-----NN	289
CpI	VTGKHYTALRQLGFDKSFEDINFGADMTHFEEAEEVNEE-----NN	290
Dd	TTGKMLAALQKLCFAHCWDTTEFTADVTIWEEGSERVERLT-----KSD	142
CrHydA2	SPGKMATGLRAEGFEDQFETLHAKL-----HREKEHLEAHPHSD	163
CrHydA1	TPKQLAEGLRLGFDDEVFDTLFGADLTIMPEGSELHRETEHLEAHPHSD	160
CaI	GPEPMFTSCCPAWVRLAQNYHPELDNESSAKSPQQIFGTASKTYYPSIS	339
CpI	GPEPMFTSCCPGWWRQENYEPRLNNSSAKSPQQIFGTASKTYYPSIS	340
Dd	MPEPQFTSCCPGWQKYAETYYPELPHFSTICKSPIGMNGALAKTYGAERM	192
CrHydA2	EPLPMFTSCCPGWVAMMEKSYPELPPFVSSCKSPQMMMGAMVKTYLSEKQ	213
CrHydA1	EPLPMFTSCCPGWIAMEEKSYPEPDITPYVSSCKSPQMMLAAMVKSYLAEKK	210
CaI	GLAPEDVYTVTIPCPNDKKYEADIPFMETNS---LRDIDASLTTRRELAKM	386
CpI	GLDPKNVFTVTPVMPCTSKKFEADRPQMEKDG---LRDIDAVITTRRELAKM	387
Dd	KYDPKQVYTVSIMPICIAKKYEGLRPELKSSG---MRDIDATEETTRELAYM	239
CrHydA2	GTPAKDTVMVSVMPCVRKQGEADREWFCVSE-PGVRDVDHVITTAELGNI	262
CrHydA1	GLAPKDMVMVSVIMPCTRQKSEADRDWFCVDADPTLRQLDHVITVELGNI	260
CaI	EKDAKIKFADLEDGEVDPAMGTYSGAGATFGATGGVMEAAIRSAKDEAEN	436
CpI	EKDAKIKIPFAKLEDSEADPAMGEYSAGATFGATGGVMEAAIRSAKDEAEN	437
Dd	EKKAGIDFAKLPDGKRDLSLMGESSTGGATTFGVTGGVMEAAIRFAYEAVTG	289
CrHydA2	EKERGINLPELPDSDWQPLGLGSAGVLFGTTGGVMEAAIRFAYEELVTK	312
CrHydA1	EKERGINLAELPEGEDWDNPMSGVGSAGVLFGTTGGVMEAAIRFAYEELFTG	310
CaI	KELENVDYTEVRGFKGIKEAEVET-----	461
CpI	AELEDFEYKQVVRGELNGIKAEEVEEN-----	462
Dd	KKPDWSDFKAVRGEDGIKEATVNNG-----	314
CrHydA2	EPLPRLNLSEVRGLEDGIKEASVTEVPAPGSKFAELVAERLAHKVEAAAA	362
CrHydA1	TPPLPRLSLSEVRGMDGIKETNETMVPAPGSKFEELLKHRAAARAEAAAHG	360
CaI	-----GNKENVAVINGASNFFEFMKS	482
CpI	-----NNKYNVAVINGASNLFKFMKS	483
Dd	-----GTDVKVAVVHGAKRFKQVCD	335
CrHydA2	AAAAAVEGAVKPPIAVDGGQGFSTDDGKGGLKLRVAVANGLGNAKKELIGK	412
CrHydA1	TPG-----PLAWDGGAGFTSEDGRGGITLERVAVANGLGNAKKLITK	401
CaI	GKMNKEKQYHFTEVMACPGGCGINGGGQPHVNALDRENVDYRKLRAHSVLYNQ	532
CpI	GMINKEKQYHFTEVMACPGGCGVNGGQPHVNPKDLEKVDIKKVRASVLYNQ	533
Dd	VKAGKSPYHFTEVMACPGGCGVCGGGQPHVMPGVLEA-----	370
CrHydA2	MVSGEAKYDFVEIMACPAGCVGGGGQPRSTDKQITQK-----RQAALYDL	457
CrHydA1	MQAGEAKYDFVEIMACPAGCVGGGGQPRSTDKAITQK-----RQAALYNL	446

Fig. 1A

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Fig. 1B

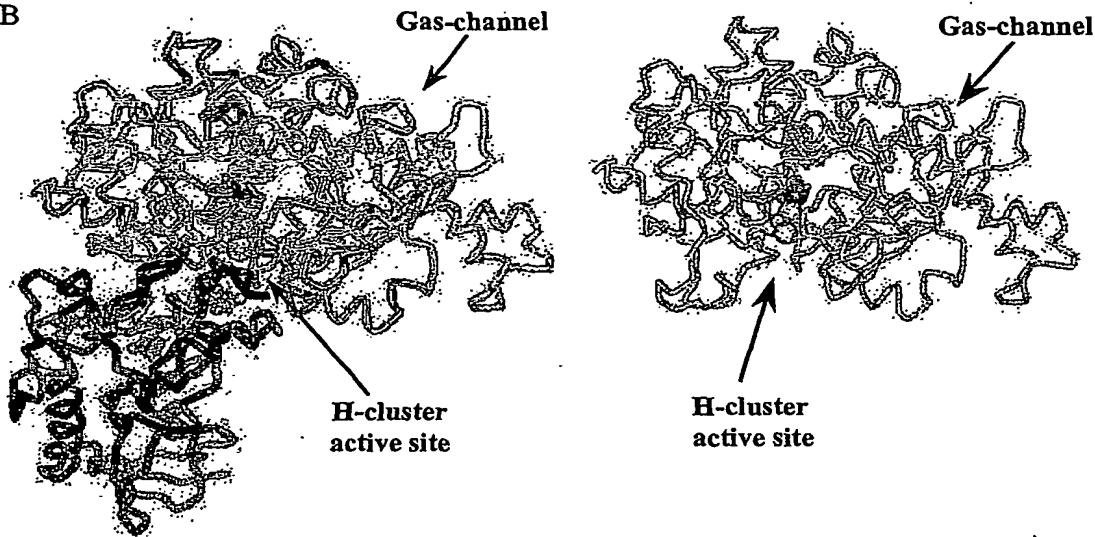
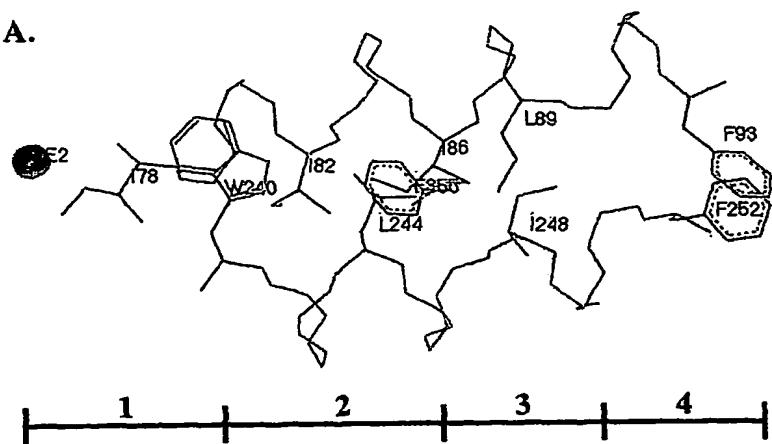
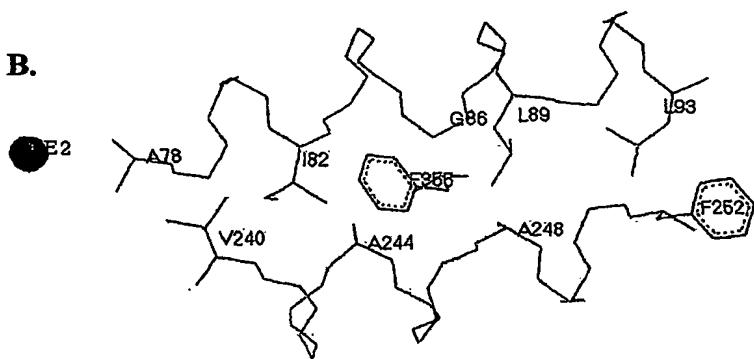
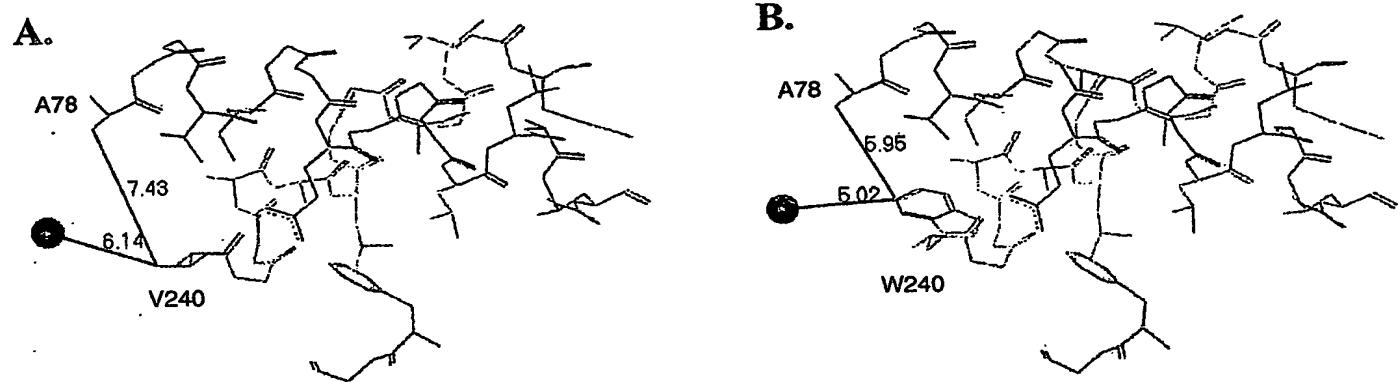
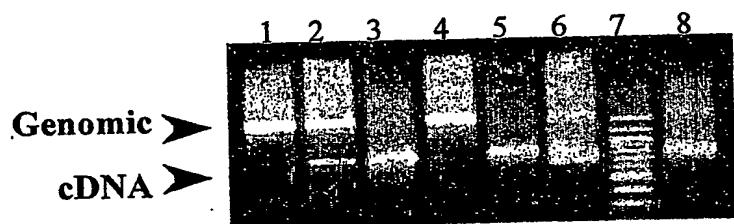
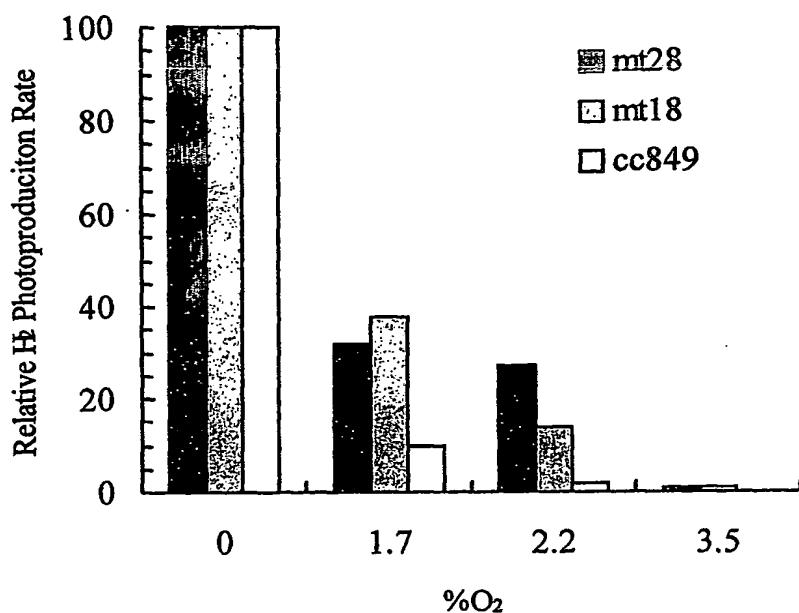
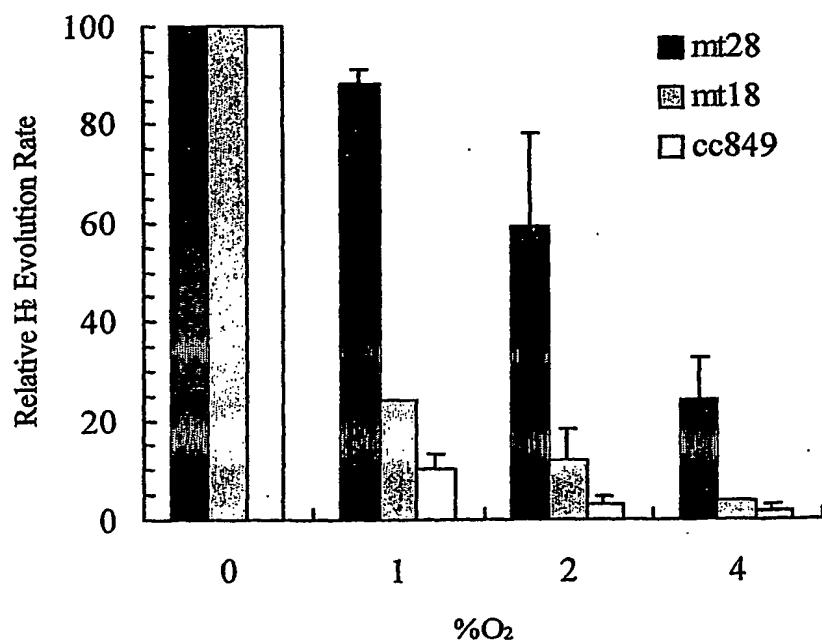


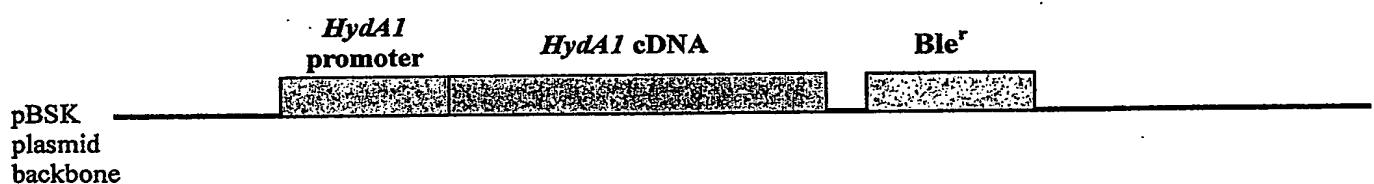
Fig. 2

Cr HydA1	AAPAAEAPLSHVQQALAEELAKPKDDPTRKHVCVQVAPAVRAIAETLGLAPGATTPKQLA	60
CpI	CIIACPVAALSEKSHMDRVKNALNAPKHVIVAMAPSVRASIGELFNMGFGVDVTGKIY	59
<hr/>		
Cr HydA1	EGLRLIGFDEVFDTLFGADLTIMEE	120
CpI	<del>EGLRLIGFDEVFDTLFGADLTIMEE</del> SELHRPTEDEPLPMFTSCCPGWIAMLEKSYPDL	119
TALRQLGFDKIFDINF	GADMTIMEE	
<hr/>		
Cr HydA1	IPYVSSCKSPQMMILAAMVKSYLAEKKGIAPKDMVMVSIMPCTRQSEADRDWFCVDADPT	180
CpI	LNNLSSAKSPQQIFGTASKTYYPSISGLDPKNVFTVTVMPCSTSKKFEADRPQMEKDG---	176
<hr/>		
Cr HydA1	LRQLDHVITTVELGNIFKERGINLAELEPEGEWDNPMSGVSGAGVLFGTTGG	240
CpI	LRDIDAVITTRELAKMIKDAKIPFAKLEDSEADPAMGEYSGAGAIFGATGG	236
<hr/>		
Cr HydA1	Y <del>ME</del> TGTPLPLRLSILSEVRGMGDIKETNITMVPATLR <del>VAV</del> <sup>←</sup> NGLGNNAKKLITKMQAGEAKY	300
CpI	KDE <del>ME</del> ENAELEDIEYKQVRGLNGIKEAEVEINNNKYN <del>VAV</del> <sup>←</sup> NGASNLFKFMKSGMINEKQY	296
<hr/>		
Cr HydA1	D <del>ME</del> MACPAGCVGGGGQPRSTDKAITQKRQAALYNLDEKSTLRRSHENPSIRELYDTYL	360
CpI	H <del>ME</del> MACHGGCVGGGQPHVNPKDIKKVRAVLYNQDEHLSKRKSHENTALVKMYQNYF	356
<hr/>		
Cr HydA1	GEPLGHKAHELLHTHYVAGGVEEKDEKK	388
CpI	GKPGEGRAHEILHFKYKK-----	374

**Fig. 3****A.****B.**

**Fig. 4****Fig. 5**

**Fig. 6****H<sub>2</sub> Electrode Assay****Fig. 7****MV Assay**

**Fig. 8****Fig. 9**

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